

[illegible]

AA074579
AA074579
PAP.
human.
Homo sapiens

REFERENCE	1 (base)
AUTHOR(S)	H. J. CAN
TITLE	National
JOURNAL	Tumor Act
COMMENT	unpublished
	Contact :

$$\text{FET}(\text{A} \mid \text{B}, \text{S})$$

PAGE CONT.

PROPERTY MANAGEMENT

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099																																																																																																																																																																																																																																						
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Dd	170	G;AAG;ACGCG

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DB	111	TGTCACACG			
W	1680	CTGCTGCTTT			

[illegible]

RESULT 7
RQ773718/c
LAWREN
DEFINITION

KEYWORDS:
SOURCE:
ORIGIN:

FEATURES

BASE POINT
ORIGIN

1085
 1086
 1087

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Q1 1971

cDNA Library Preparation: M. Rong, Sources, Phila.
cDNA Library Arrayed by: Greg Kennedy, Phila.
DNA Sequencing by: Washington University Genome Sequencing Center
Close distibution: NCICAP close distibution information can be
found through the L.M.A.CAP, contact form/LENC at:
www.lmcap.org, 644-2222, or e-mail
lenc@lmcap.org
Insert length: 622 Std Error: 600

FINANCIAL

 $\frac{d}{dt}$

1. 1.

Signature/

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Collection of "N": "NAT. KIN."

[illegible]

Curtis, " - " - " = Kidline

with a modified polybrene-GITC¹¹ No. 12 (Sigma) kit. Cells were transfected with the recombinant library. The library was prepared, and ss cDNAs were made *in vitro*. Following purification, this cDNA was used as target in a subsequent hybridization reaction. The driver was help amplified cDNAs from a pool of 5,000 clones made from the same library (accession 132274, 1327911, 135007, 1356775, and 1350552, 1352855). Subtraction by Benton Soares and M. J. Mattingly.

\mathbb{Z}
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References

[illegible]
$$S_1 \rightarrow S_2 \rightarrow \dots \rightarrow S_n \rightarrow S_{n+1} \rightarrow \dots$$
[illegible]

2017-01-17 10:10:10

[illegible][illegible][illegible]
$$211 \quad \Gamma_1 \Gamma_2 \Gamma_3 \Gamma_4 \Gamma_5 \Gamma_6 \Gamma_7 \Gamma_8 \Gamma_9 \Gamma_{10} \Gamma_{11} \Gamma_{12} \Gamma_{13} \Gamma_{14} \Gamma_{15} \Gamma_{16} \Gamma_{17} \Gamma_{18} \Gamma_{19} \Gamma_{20} \Gamma_{21} \Gamma_{22} \Gamma_{23} \Gamma_{24} \Gamma_{25} \Gamma_{26} \Gamma_{27} \Gamma_{28} \Gamma_{29} \Gamma_{30} \Gamma_{31} \Gamma_{32} \Gamma_{33} \Gamma_{34} \Gamma_{35} \Gamma_{36} \Gamma_{37} \Gamma_{38} \Gamma_{39} \Gamma_{40} \Gamma_{41} \Gamma_{42} \Gamma_{43} \Gamma_{44} \Gamma_{45} \Gamma_{46} \Gamma_{47} \Gamma_{48} \Gamma_{49} \Gamma_{50} \Gamma_{51} \Gamma_{52}$$
[illegible]

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$$|\psi\rangle = \frac{1}{\sqrt{2}} \left[\left(\frac{1}{\sqrt{2}} \left(|\psi_1\rangle + |\psi_2\rangle \right) \right) \otimes \left(\frac{1}{\sqrt{2}} \left(|\psi_1\rangle + |\psi_2\rangle \right) \right) + \left(\frac{1}{\sqrt{2}} \left(|\psi_1\rangle - |\psi_2\rangle \right) \right) \otimes \left(\frac{1}{\sqrt{2}} \left(|\psi_1\rangle - |\psi_2\rangle \right) \right) \right]$$
$$\mathcal{A}_n = \{A_1, \dots, A_n\} \subseteq \mathcal{A} \text{ is a } \mathcal{A}\text{-}n\text{-system if and only if } \mathcal{A}_n \text{ is a } \mathcal{A}\text{-}n\text{-system.}$$
[illegible]
$$|k\rangle = \frac{1}{\sqrt{N}} \sum_{j=0}^{N-1} e^{-ikja} |j\rangle$$

5

Figure 1. The effect of the concentration of the Ca^{2+} solution on the Ca^{2+} concentration in the Ca^{2+} solution. The concentration of the Ca^{2+} solution was 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2.0, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3.0, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4.0, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6.0, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7.0, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8.0, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9.0, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, 10.0, 10.1, 10.2, 10.3, 10.4, 10.5, 10.6, 10.7, 10.8, 10.9, 11.0, 11.1, 11.2, 11.3, 11.4, 11.5, 11.6, 11.7, 11.8, 11.9, 12.0, 12.1, 12.2, 12.3, 12.4, 12.5, 12.6, 12.7, 12.8, 12.9, 13.0, 13.1, 13.2, 13.3, 13.4, 13.5, 13.6, 13.7, 13.8, 13.9, 14.0, 14.1, 14.2, 14.3, 14.4, 14.5, 14.6, 14.7, 14.8, 14.9, 15.0, 15.1, 15.2, 15.3, 15.4, 15.5, 15.6, 15.7, 15.8, 15.9, 16.0, 16.1, 16.2, 16.3, 16.4, 16.5, 16.6, 16.7, 16.8, 16.9, 17.0, 17.1, 17.2, 17.3, 17.4, 17.5, 17.6, 17.7, 17.8, 17.9, 18.0, 18.1, 18.2, 18.3, 18.4, 18.5, 18.6, 18.7, 18.8, 18.9, 19.0, 19.1, 19.2, 19.3, 19.4, 19.5, 19.6, 19.7, 19.8, 19.9, 20.0, 20.1, 20.2, 20.3, 20.4, 20.5, 20.6, 20.7, 20.8, 20.9, 21.0, 21.1, 21.2, 21.3, 21.4, 21.5, 21.6, 21.7, 21.8, 21.9, 22.0, 22.1, 22.2, 22.3, 22.4, 22.5, 22.6, 22.7, 22.8, 22.9, 23.0, 23.1, 23.2, 23.3, 23.4, 23.5, 23.6, 23.7, 23.8, 23.9, 24.0, 24.1, 24.2, 24.3, 24.4, 24.5, 24.6, 24.7, 24.8, 24.9, 25.0, 25.1, 25.2, 25.3, 25.4, 25.5, 25.6, 25.7, 25.8, 25.9, 26.0, 26.1, 26.2, 26.3, 26.4, 26.5, 26.6, 26.7, 26.8, 26.9, 27.0, 27.1, 27.2, 27.3, 27.4, 27.5, 27.6, 27.7, 27.8, 27.9, 28.0, 28.1, 28.2, 28.3, 28.4, 28.5, 28.6, 28.7, 28.8, 28.9, 29.0, 29.1, 29.2, 29.3, 29.4, 29.5, 29.6, 29.7, 29.8, 29.9, 30.0, 30.1, 30.2, 30.3, 30.4, 30.5, 30.6, 30.7, 30.8, 30.9, 31.0, 31.1, 31.2, 31.3, 31.4, 31.5, 31.6, 31.7, 31.8, 31.9, 32.0, 32.1, 32.2, 32.3, 32.4, 32.5, 32.6, 32.7, 32.8, 32.9, 33.0, 33.1, 33.2, 33.3, 33.4, 33.5, 33.6, 33.7, 33.8, 33.9, 34.0, 34.1, 34.2, 34.3, 34.4, 34.5, 34.6, 34.7, 34.8, 34.9, 35.0, 35.1, 35.2, 35.3, 35.4, 35.5, 35.6, 35.7, 35.8, 35.9, 36.0, 36.1, 36.2, 36.3, 36.4, 36.5, 36.6, 36.7, 36.8, 36.9, 37.0, 37.1, 37.2, 37.3, 37.4, 37.5, 37.6, 37.7, 37.8, 37.9, 38.0, 38.1, 38.2, 38.3, 38.4, 38.5, 38.6, 38.7, 38.8, 38.9, 39.0, 39.1, 39.2, 39.3, 39.4, 39.5, 39.6, 39.7, 39.8, 39.9, 40.0, 40.1, 40.2, 40.3, 40.4, 40.5, 40.6, 40.7, 40.8, 40.9, 41.0, 41.1, 41.2, 41.3, 41.4, 41.5, 41.6, 41.7, 41.8, 41.9, 42.0, 42.1, 42.2, 42.3, 42.4, 42.5, 42.6, 42.7, 42.8, 42.9, 43.0, 43.1, 43.2, 43.3, 43.4, 43.5, 43.6, 43.7, 43.8, 43.9, 44.0, 44.1, 44.2, 44.3, 44.4, 44.5, 44.6, 44.7, 44.8, 44.9, 45.0, 45.1, 45.2, 45.3, 45.4, 45.5, 45.6, 45.7, 45.8, 45.9, 46.0, 46.1, 46.2, 46.3, 46.4, 46.5, 46.6, 46.7, 46.8, 46.9, 47.0, 47.1, 47.2, 47.3, 47.4, 47.5, 47.6, 47.7, 47.8, 47.9, 48.0, 48.1, 48.2, 48.3, 48.4, 48.5, 48.6, 48.7, 48.8, 48.9, 49.0, 49.1, 49.2, 49.3, 49.4, 49.5, 49.6, 49.7, 49.8, 49.9, 50.0, 50.1, 50.2, 50.3, 50.4, 50.5, 50.6, 50.7, 50.8, 50.9, 51.0, 51.1, 51.2, 51.3, 51.4, 51.5, 51.6, 51.7, 51.8, 51.9, 52.0, 52.1, 52.2, 52.3, 52.4, 52.5, 52.6, 52.7, 52.8, 52.9, 53.0, 53.1, 53.2, 53.3, 53.4, 53.5, 53.6, 53.7, 53.8, 53.9, 54.0, 54.1, 54.2, 54.3, 54.4, 54.5, 54.6, 54.7, 54.8, 54.9, 55.0, 55.1, 55.2, 55.3, 55.4, 55.5, 55.6, 55.7, 55.8, 55.9, 56.0, 56.1, 56.2, 56.3, 56.4, 56.5, 56.6, 56.7, 56.8, 56.9, 57.0, 57.1, 57.2, 57.3, 57.4, 57.5, 57.6, 57.7, 57.8, 57.9, 58.0, 58.1, 58.2, 58.3, 58.4, 58.5, 58.6, 58.7, 58.8, 58.9, 59.0, 59.1, 59.2, 59.3, 59.4, 59.5, 59.6, 59.7, 59.8, 59.9, 60.0, 60.1, 60.2, 60.3, 60.4, 60.5, 60.6, 60.7, 60.8, 60.9, 61.0, 61.1, 61.2, 61.3, 61.4, 61.5, 61.6, 61.7, 61.8, 61.9, 62.0, 62.1, 62.2, 62.3, 62.4, 62.5, 62.6, 62.7, 62.8, 62.9, 63.0, 63.1, 63.2, 63.3, 63.4, 63.5, 63.6, 63.7, 63.8, 63.9, 64.0, 64.1, 64.2, 64.3, 64.4, 64.5, 64.6, 64.7, 64.8, 64.9, 65.0, 65.1, 65.2, 65.3, 65.4, 65.5, 65.6, 65.7, 65.8, 65.9, 66.0, 66.1, 66.2, 66.3, 66.4, 66.5, 66.6, 66.7, 66.8, 66.9, 67.0, 67.1, 67.2, 67.3, 67.4, 67.5, 67.6, 67.7, 67.8, 67.9, 68.0, 68.1, 68.2, 68.3, 68.4, 68.5, 68.6,

Genome version 6.1.4_p5_4578
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ORF nucleotide sequence search using SW model

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(without alignments)
15709,302 hit(s) on cell updates/sec

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Gapop 10.0 ; Gapext 1.9
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Minimum hit seq length: 0
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Listed first 45 summaries

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Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the best hit found printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Accession
1	1727	100.0	1727	6	AX074572	AX074572 Sequence
2	611.36	35.4	1376	9	U018995	U018995 Homo Sap1
3	498	26.8	498	6	AX073662	AX073662 Sequence
4	372.34	21.6	381	6	AX073662	AX073662 Sequence
5	177.36	10.3	347	9	AK056404	AK056404 Homo Sap1
6	176	10.2	351	9	AB056807	AB056807 Mus mus
7	143.4	8.4	551	11	AC084178	AC084178 Homo Sap1
8	127.36	7.4	254	11	AC084178	AC084178 Homo Sap1
9	123.36	7.2	1376	2	AC011257	AC011257 Homo Sap1
10	107.4	6.2	2879	9	AK000723	AK000723 Homo Sap1
11	107.4	6.2	2893	6	AX056921	AX056921 Sequence
12	99.2	5.7	176287	10	AL513447	AL513447 Mouse LNA
13	96	5.6	203558	2	AC011839	AC011839 Homo Sap1
14	90	5.2	91876	9	AL512286	AL512286 Homo LNA
15	84.2	4.9	12314	2	AL512286	AL512286 Homo LNA
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17	65.8	3.8	62649	2	AC025552	AC025552 Homo Sap1
18	65.2	3.8	424	11	HS0071203	HS0071203 Homo Sap1
19	64.6	3.7	203558	2	AC011839	AC011839 Homo Sap1
20	63	3.6	76734	2	AC024218	AC024218 Homo Sap1
21	62.2	3.6	1941	6	AK04152	AK04152 Sequence
22	62.2	3.6	166742	2	AC0128817	AC0128817 Homo Sap1
23	61.2	3.5	13801	2	AC094575	AC094575 Homo Sap1
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26	60.2	3.5	51274	2	AC024454	AC024454 Homo Sap1
27	59.6	3.5	61150	2	AC0100284	AC0100284 Mus mus
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29	59.6	3.5	194242	2	AC098291	AC098291 Homo Sap1
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ALPHABET

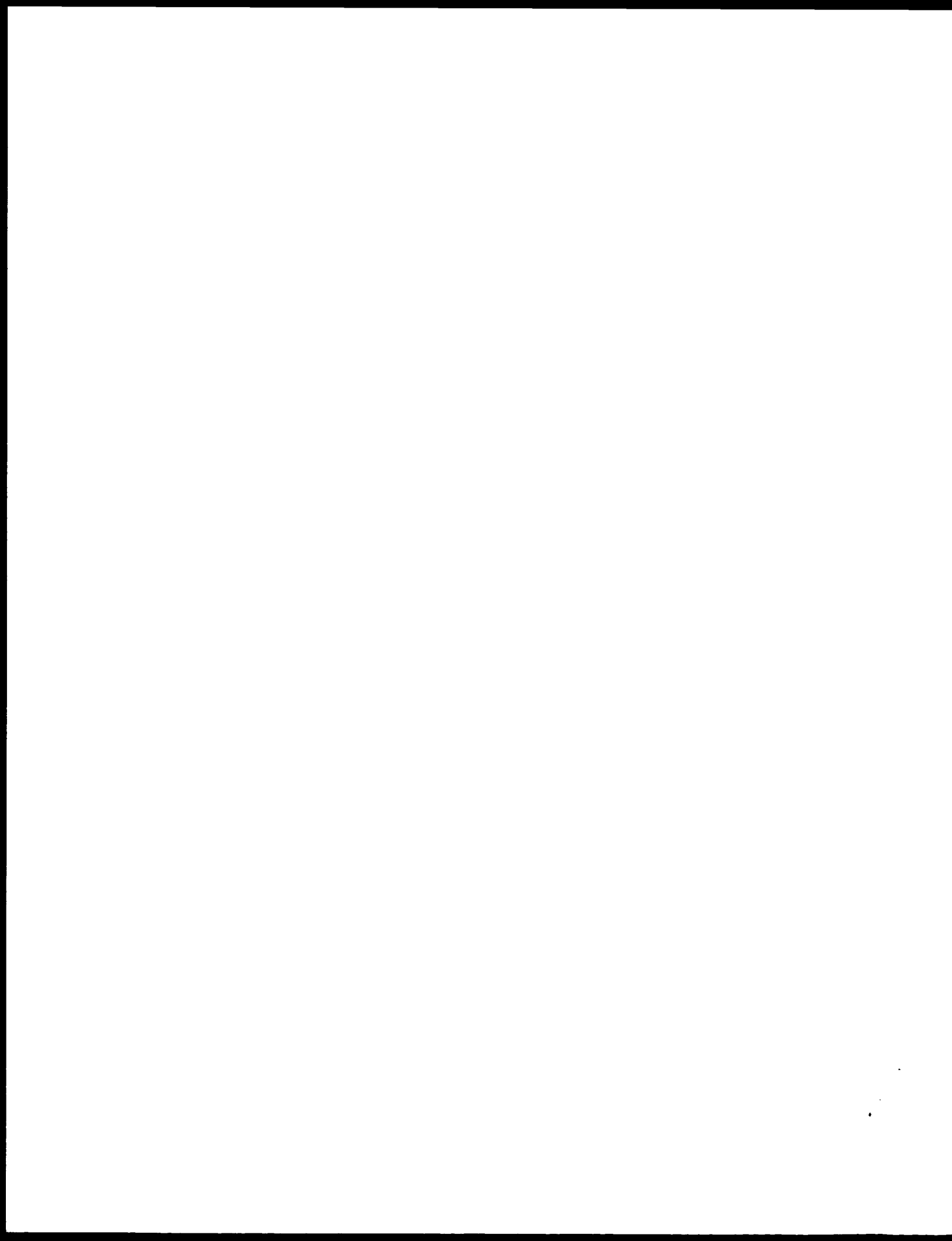
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ACCESSION	AX074572.1	GI:12709988			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					

Query Match	10,200	Score 1761	1P 97	Length 6143
Best Local Similarity	66.1%	Prod. No. 136 272		
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[illegible]

[illegible]

APPLICANT: Yano, Isamu
 APPLICANT: Matsuda, Akiro
 APPLICANT: Nakano, Hirotsugu
 APPLICANT: Ito, Koji
 TITLE: INVENTOR. Probe for Diarrhoeal Infection Disease
 NUMBER OF PAGES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, G'loster, Martin & Berni
 STREET: 6400 Stars Tower, 244 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 NUMBER READABLE FORM:
 READING TYPE: Fully Blank
 COMPUTER: IBM PC compatible
 ORIGINATING OFFICE: PC 104748 1008
 IS MACHINE: Part of the Release #1.0, Version #1.0.4
 CURRENT AND FINAL DATA:
 RECEIVING NUMBER: 82/209/002, 6370
 RECEIVING DATE: 27 MAR 1995
 CLASSIFICATION:
 CLASSIFICATION NUMBER: 536
 NAME: Yano, Isamu; Ito, Koji
 RESEARCHER NUMBER: 33,547
 RECEIVING NUMBER: 82/209/002, 6370
 HEADQUARTER NUMBER: 24420
 HEADQUARTER TELEPHONE:
 TELEPHONE: 312/747-6300
 TELEFAX: 312/747-0448
 CITY: CHICAGO
 POST OFFICE NUMBER: 60606
 POST OFFICE TELEPHONE: 312/747-6300
 TELEFAX: 312/747-0448
 LENGTH: 647 base pairs
 TYPE: nucleic acid
 COMPOSITION: double
 TOPLOGY: linear
 MOLECULE TYPE: genomic DNA
 ORIGINAL SOURCE:
 ORGANISM: Escherichia coli
 STRAIN: clinical isolate P2-17



GENERAL INFORMATION:

1 APPLICANT: Zuckermann et al.
 2 TITLE OF INVENTION: Compositions and Methods for
 3 POLYNUCLEOTIDE DELIVERY
 4 NUMBER OF SEQUENCES: 4
 5 CORRESPONDENCE ADDRESS:
 6 ADDRESSEE: Chiron Corporation
 7 STREET: 4560 Horton Street
 8 CITY: Emeryville
 9 STATE: California
 10 COUNTRY: U.S.A.
 11 ZIP: 94608-2916
 12 COMPUTER READABLE FORM:
 13 MEDIUM TYPE: Floppy disk
 14 COMPUTER: IBM PC compatible
 15 OPERATING SYSTEM: PC-DOS/MS-DOS
 16 SOFTWARE: Patent In Release #1.0, Version #1.0
 17 FILING DATE: 21-Jul-2000
 18 CLASSIFICATION: Unknown
 19 ATTORNEY/AGENT INFORMATION:
 20 NAME: Follis, Sharon M.
 21 REGISTRATION NUMBER: 38,459
 22 REFERENCE/DECK NUMBER: 1218.002
 23 TELECOMMUNICATION INFORMATION:
 24 TELEPHONE: (510) 924-2706
 25 TELEFAX: (510) 655-4542
 26 INFORMATION FOR SEQ ID NO: 1:
 27 SEQUENCE CHARACTERISTICS:
 28 LENGTH: 9600 base pairs
 29 TYPE: nucleic acid
 30 STRANDEDNESS: single
 31 TOPOLOGY: linear
 32 MOLECULE TYPE: DNA (genomic)

US 09 620 925 1

Query Match: 3.18; Score 53.2; PB 4; Length 9600
 Best Local Similarity: 45.88; Pred. No. 0.00018;
 Matches: 219; Conservative: 0; Mismatches: 258; Indels: 1; Gaps: 1;
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 BB 1541 CAGCTGTAATCTGTGACATCTATGCTGAGGAGGACAGACCCCTGGGCGCTACTA 950
 QY 951 CAGCTGTAATCTGTGACATCTATGCTGAGGAGGACAGACCCCTGGGCGCTACTA 1010
 BB 1481 CAGCTGTAATCTGTGACATCTATGCTGAGGAGGACAGACCCCTGGGCGCTACTA 1422
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 QY 1367 CAGCTGTAATCTGTGACATCTATGCTGAGGAGGACAGACCCCTGGGCGCTACTA 1367
 BB 1121 CAGCTGTAATCTGTGACATCTATGCTGAGGAGGACAGACCCCTGGGCGCTACTA 1064

RESULT 9

09 620 925 1/3
 1 Sequence 1: Application no/09620925
 2 Patent No. 6469986
 3 CURRENT INFORMATION:
 4 APPLICANT: Zuckermann et al.
 5 TITLE OF INVENTION: Compositions and Methods for
 6 POLYNUCLEOTIDE DELIVERY
 7 NUMBER OF SEQUENCES: 4
 8 CORRESPONDENCE ADDRESS:
 9 ADDRESSEE: Chiron Corporation
 10 STREET: 4560 Horton Street
 11 CITY: Emeryville
 12 STATE: California
 13 COUNTRY: U.S.A.
 14 ZIP: 94608-2916
 15 COMPUTER READABLE FORM:
 16 MEDIUM TYPE: Floppy disk
 17 COMPUTER: IBM PC compatible
 18 OPERATING SYSTEM: PC-DOS/MS-DOS
 19 SOFTWARE: Patent In Release #1.0, Version #1.0
 20 FILING DATE: 21-Jul-2000
 21 CLASSIFICATION: Unknown
 22 ATTORNEY/AGENT INFORMATION:
 23 NAME: Follis, Sharon M.
 24 REGISTRATION NUMBER: 38,459
 25 REFERENCE/DECK NUMBER: 1218.002
 26 TELECOMMUNICATION INFORMATION:
 27 TELEPHONE: (510) 924-2706
 28 TELEFAX: (510) 655-4542
 29 INFORMATION FOR SEQ ID NO: 1:
 30 SEQUENCE CHARACTERISTICS:
 31 LENGTH: 9600 base pairs
 32 TYPE: nucleic acid
 33 STRANDEDNESS: single
 34 TOPOLOGY: linear
 35 MOLECULE TYPE: DNA (genomic)

US-09-620-925 1

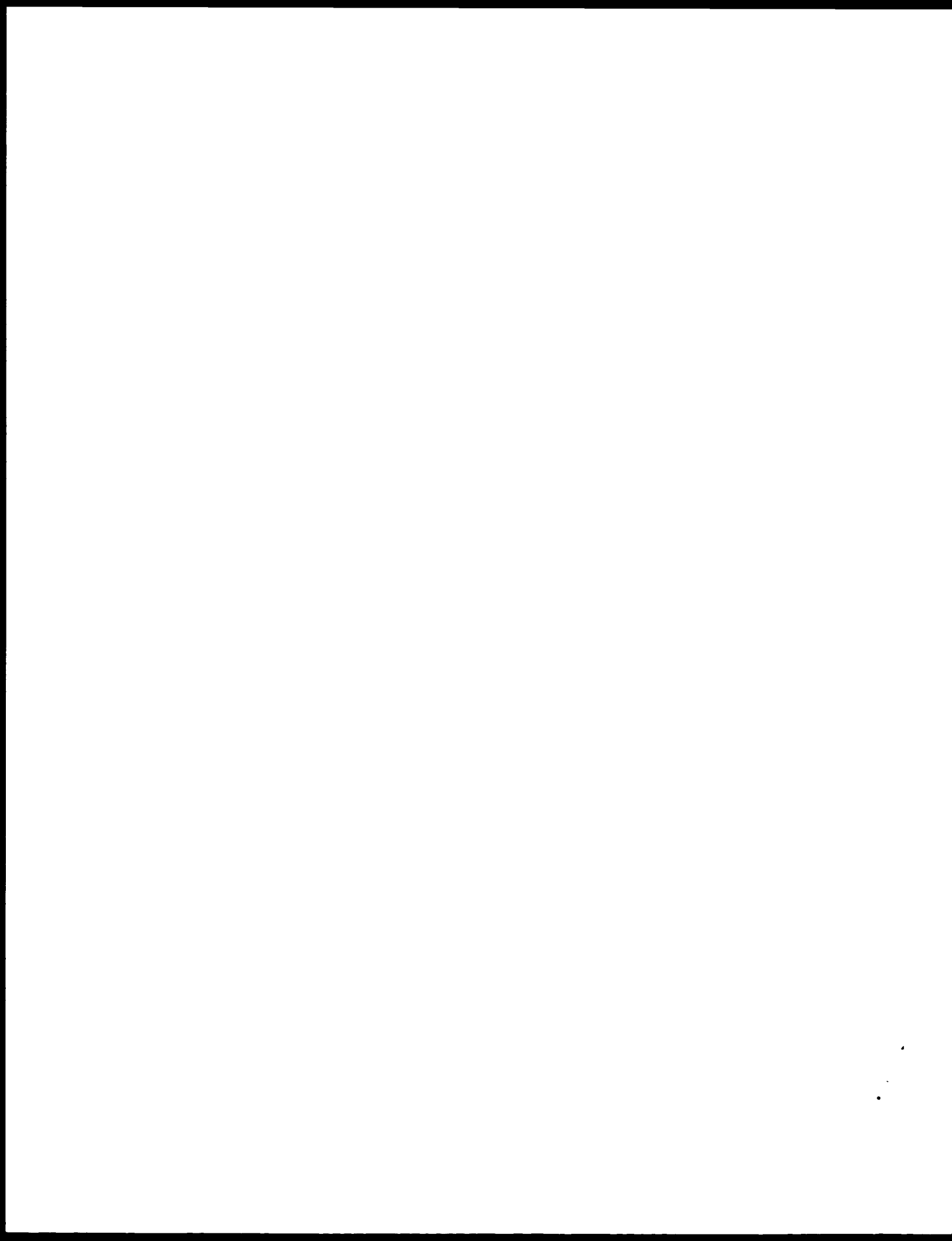
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1 FILE REFERENCE: PA113
2 CURRENT FILING DATE: 2001-01-17
3 PRIOR APPLICATION DATA REMOVED : CONSULT PALM OF FILE SHEET
4 NUMBER OF SEQ ID NOS: 658
5 SOFTWARE: Patent In Ver. 2.0
6 SEQ ID NO: 123
7 LENGTH: 456
8 TYPE: DNA
9 ORGANISM: Homo sapiens
10 59 74 83 123
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12 Seq. Data:
13 Best Local Similarity: 6.78; Score: 33.4; DR: 10; Length: 456;
14 Seq Id: 59; Cons: 74; Mismatches: 0; Gaps: 0
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16 658 SEQ ID NOS: 123-658
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18 66 SEQ ID NOS: 123-658
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20 305 GENE: 123-658
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26 RESULT 7
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28 OS-09-7-38-626-654
29
30 Sequence: 658; Application: 95/05739626
31 Publication No.: US20020197005A1
32 GENERAL INFORMATION:
33 APPLICANT: NAKAMURA, SAIO SHI
34 APPLICANT: HIRAKAWA, HIROSHI
35 APPLICANT: ANDO, SEIKO
36 APPLICANT: HANASHI, KEIKO
37 APPLICANT: YOKOI, HADZUKO
38 APPLICANT: ABE, HIROSHI, NAKO
39 APPLICANT: SHIBU, AKIHIRO
40 APPLICANT: KIKAWA, MASAO
41 APPLICANT: OKADA, AKIO
42 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
43 FILE REFERENCE: 249-125
44
45 658 SEQ ID NOS: 123-658
46
47 CURRENT FILING DATE: 2000-12-18
48 PRIOR APPLICATION NUMBER: JP 99/477484
49 PRIOR FILING DATE: 1999-12-16
50 PRIOR APPLICATION NUMBER: JP 99/159162
51 PRIOR FILING DATE: 2000-04-07
52 PRIOR APPLICATION NUMBER: JP 99/280998
53 PRIOR FILING DATE: 2000-08-04
54 NUMBER OF SEQ ID NOS: 7059
55 SOFTWARE: Patent In Ver. 3.0
56 SEQ ID NO: 654
57 LENGTH: 655
58 TYPE: DNA
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60 658 SEQ ID NOS: 123-658
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62 OS-09-7-38-626-654
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QY 242 GAGAGGAAATGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 301
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DEFINITION mRNA sequence.
ACCESSION M1550456
VERSION M1550456.1 GI:15447608
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 696)
NIH-MGC http://mgi.scripps.edu/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straussberg, Ph.D.
Email: rstrauss@mit.edu
Tissue Procurement: Miklos Palkevičius, M.D., Ph.D.,
cDNA Library Preparation: Michael J. Brownstein (NIHDC), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIND)
cDNA Sequencing by: Tocyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIND at:
http://image.lind.org
Plates: IMAGE606, row: c, column: 09
High quality suspension stock: 69%.
Location/Qualifiers
1..696
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Zdb-Xref "taxon:606"
Zclone "IMAGE:5264240"
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Znote "organ: brain; Vector: pBluescriptR (modified
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for full length clones and constructed using the
cap trapped method (Carninci, in preparation). Library
constructed by M. Brownstein (NIHDC/Riken). National
Institutes of Health). Note: This is a NIH_MGC Library."
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Query Match

30.58; Score 166.6; DB 13; Length 696;

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